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# UniProtKB/Swiss-Prot entry Q69ZS6

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## Entry information

Entry name	SV2C_MOUSE
Primary accession number	Q69ZS6
Secondary accession numbers	None
Integrated into Swiss-Prot on	June 13, 2006
Sequence was last modified on	June 13, 2006 (Sequence version 2)
Annotations were last modified on	June 10, 2008 (Entry version 32)
Name and origin of the protein	
Protein name	Synaptic vesicle glycoprotein 2C
Synonym	Synaptic vesicle protein 2C
Gene name	Name: Sv2c Synonyms: Kiaa1054
From	Mus musculus (Mouse) [TaxID: 10090]
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Gli Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; M
Protein existence	1: Evidence at protein level;

## References

### [1] NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

TISSUE=Fetal brain;

DOI=10.1093/dnares/11.3.205; PubMed=15368895 [NCBI, ExPASy, EBI, Israel, Japan]

Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S., Saga Y., Seino S., Nishimura M., Kaisho T., Hoshino K., Kitamura H., Nagase T., Ohara O., Koga H.;

"Prediction of the coding sequences of mouse homologues of KIAA gene: IV. The complete nucleotide sequences of 500 mouse KIAA-homologous cDNAs identified by screening of terminal sequences of cDNA clones randomly sampled from size-fractionated libraries."; DNA Res. 11:205-218(2004).

[2] INDUCTION.

DOI=10.1038/35087000; PubMed=11483953 [NCBI, ExPASy, EBI, Israel, Japan]

Xu T., Bajjalieh S.M.;

"SV2 modulates the size of the readily releasable pool of secretory vesicles.;"

Nat. Cell Biol. 3:691-698(2001).

[3] TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.

DOI=10.1002/cne.10636; PubMed=12687700 [NCBI, ExPASy, EBI, Israel, Japan]

Wang M.M., Janz R., Belizaire R., Frishman L.J., Sherry D.M.;

"Differential distribution and developmental expression of synaptic vesicle protein 2 isoform in the mouse retina.;"

J. Comp. Neurol. 460:106-122(2003).

[4] FUNCTION AS A BOTA RECEPTOR.

DOI=10.1016/j.febslet.2006.02.074; PubMed=16545378 [NCBI, ExPASy, EBI, Israel, Japan]

Mahrhold S., Rummel A., Bigalke H., Davletov B., Binz T.;

"The synaptic vesicle protein 2C mediates the uptake of botulinum neurotoxin A into phrenic nerves.;"

FEBS Lett. 580:2011-2014(2006).

[5] FUNCTION AS A BOTA RECEPTOR.

DOI=10.1126/science.1123654; PubMed=16543415 [NCBI, ExPASy, EBI, Israel, Japan]

Dong M., Yeh F., Tepp W.H., Dean C., Johnson E.A., Janz R., Chapman E.R.;

"SV2 is the protein receptor for botulinum neurotoxin A.;"

Science 312:592-596(2006).

Comments

- **FUNCTION:** Plays a role in the control of regulated secretion in neural and endocrine cells by enhancing selectively low-frequency neurotransmission. Positively regulates vesicle fusion by maintaining the readily releasable pool of secretory vesicles (*By similarity*).
- **FUNCTION:** Receptor for the botulinum neurotoxin type A/BOTA.
- **SUBUNIT:** Interacts with SYT1 in a calcium-dependent manner (*By similarity*).
- **SUBCELLULAR LOCATION:** Cytoplasmic vesicle, secretory vesicle, synaptic vesicle, membrane; Multi-pass membrane protein (*By similarity*). Note=Enriched in small synaptic vesicles and adrenal microsomes, not present in chromaffin granules. Associated with insulin granules and synaptic-like microvesicles in insulin-secreting cells of the pancreas (*By similarity*).
- **TISSUE SPECIFICITY:** Expressed in specific subsets of conventional synapses in the retina (at protein level).
- **DEVELOPMENTAL STAGE:** Expressed during synaptogenesis in the retina (at protein level).
- **INDUCTION:** Up-regulated upon Sv2a depletion.
- **PTM:** N-glycosylated (*By similarity*).
- **SIMILARITY:** Belongs to the major facilitator superfamily.

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## Cross-references

## Sequence databases

EMBL	AK173092; BAD32370.1; ALT_INIT; mRNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
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RefSeq	XP_996351.1; -.
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UniGene	Mm.441155
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## 3D structure databases

ModBase	Q69ZS6.
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## Organism-specific databases

MGI	MGI:1922459; Sv2c.
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GeneLynx	Sv2c; Mus musculus.
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## Gene expression databases

ArrayExpress	Q69ZS6; -.
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CleanEx	MM_SV2C; -.
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GermOnline	ENSMUSG00000051111; Mus musculus.
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## Ontologies

	GO:0008021; Cellular component: synaptic vesicle ( <i>inferred from direct assay MGI</i> ).
GO	GO:0007268; Biological process: synaptic transmission ( <i>traceable author state from MGI</i> ).
	QuickGo view.

## Family and domain databases

	IPR007114; MFS.
InterPro	IPR011701; MFS_1. IPR005988; SV2. Graphical view of domain structure.
PANTHER	PTHR11600:SF32; SV2; 1.
Pfam	PF07690; MFS_1; 1. Pfam graphical view of domain structure.
TIGRFAMs	TIGR01299; synapt_SV2; 1.
PROSITE	PS50850; MFS; 1. PROSITE graphical view of domain structure (profiles).
BLOCKS	Q69ZS6.

## Genome annotation databases

Ensembl	ENSMUSG00000051111; Mus musculus. [Contig view]
GeneID	75209; -.
NMPDR	fig10090.3.peg.28276; -.

## Phylogenomic databases

HOVERGEN	Q69ZS6; -.
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## Other

SOURCE	Sv2c; Mus musculus.
ROUGE	KIAA1054.

ProtoNet Q69ZS6.

UniRef View cluster of proteins with at least 50% / 90% / 100% identity.

## Keywords

Cell junction; Cytoplasmic vesicle; Glycoprotein; Membrane; Neurotransmitter transporter; Receptor; Synapse; Transmembrane; Transport.

## Features



Feature table viewer



Feature aligner

Key	From	To	Length	Description	FTId
CHAIN	1	727	727	Synaptic vesicle glycoprotein 2C.	PRO_000023977
TOPO_DOM	1	154	154	Cytoplasmic (Potential).	
TRANSMEM	155	175	21	Potential.	
TOPO_DOM	176	191	16	Extracellular (Potential).	
TRANSMEM	192	212	21	Potential.	
TOPO_DOM	213	226	14	Cytoplasmic (Potential).	
TRANSMEM	227	247	21	Potential.	
TOPO_DOM	248	248	1	Extracellular (Potential).	
TRANSMEM	249	269	21	Potential.	
TOPO_DOM	270	280	11	Cytoplasmic (Potential).	
TRANSMEM	281	301	21	Potential.	
TOPO_DOM	302	320	19	Extracellular (Potential).	
TRANSMEM	321	341	21	Potential.	
TOPO_DOM	342	437	96	Cytoplasmic (Potential).	
TRANSMEM	438	458	21	Potential.	
TOPO_DOM	459	578	120	Extracellular (Potential).	
TRANSMEM	579	599	21	Potential.	
TOPO_DOM	600	609	10	Cytoplasmic (Potential).	
TRANSMEM	610	630	21	Potential.	
TOPO_DOM	631	636	6	Extracellular (Potential).	
TRANSMEM	637	657	21	Potential.	
TOPO_DOM	658	670	13	Cytoplasmic (Potential).	
TRANSMEM	671	693	23	Potential.	
TOPO_DOM	694	697	4	Extracellular (Potential).	
TRANSMEM	698	716	19	Potential.	
TOPO_DOM	717	727	11	Cytoplasmic (Potential).	
REGION	1	57	57	Interaction with SY11 (By similarity).	
REGION	529	566	38	BOTA-binding (By similarity).	
CARBOHYD	480	480		N-linked (GlcNAc...) (Potential).	
CARBOHYD	484	484		N-linked (GlcNAc...) (Potential).	
CARBOHYD	534	534		N-linked (GlcNAc...) (Potential).	
CARBOHYD	559	559		N-linked (GlcNAc...) (Potential).	
CARBOHYD	565	565		N-linked (GlcNAc...) (Potential).	

## Sequence information

Length: 727 AA [This is the Molecular weight: 82291 Da]

length of the unprocessed precursor [This is the MW of the unprocessed precursor] CRC64: E1D78203D4E3183A is a checksum on the sequence

<u>10</u>	<u>20</u>	<u>30</u>	<u>40</u>	<u>50</u>	<u>60</u>
MEDSYKDRTS	LMKGAKDIK	EVKKQTQVKKV	NQAVDRAQDE	YTQRSYSRFQ	DEEDDDDDYYP
<u>70</u>	<u>80</u>	<u>90</u>	<u>100</u>	<u>110</u>	<u>120</u>
PGETYSGEVN	DDEGSSEATE	GHDEEDEIYE	GEYQGIPSTN	QKGDSIVSVG	QPKGDEYKDR
<u>130</u>	<u>140</u>	<u>150</u>	<u>160</u>	<u>170</u>	<u>180</u>
RELESERRAD	EEELAQQYEL	IIQECGHGRF	QWALFFVLGM	ALMADGVEVF	VVGFVLPSAE
<u>190</u>	<u>200</u>	<u>210</u>	<u>220</u>	<u>230</u>	<u>240</u>
TDLCIPNSGS	GWLGSIVYLG	MMVGAFWGG	LADKVGRKQS	LLICMSVNGF	FAFLSSFVQG
<u>250</u>	<u>260</u>	<u>270</u>	<u>280</u>	<u>290</u>	<u>300</u>
YGFFLVCRLL	SGFGIGGAIP	TVFSYFAEVL	AREKRGEHLS	WLCMFWMIGG	IYASAMAWAI
<u>310</u>	<u>320</u>	<u>330</u>	<u>340</u>	<u>350</u>	<u>360</u>
IPHYGWSFSM	GSAYQFHSWR	VFVIVCALPC	VSSVVALTFM	PESPRFLLEV	GKHDEAWMIL
<u>370</u>	<u>380</u>	<u>390</u>	<u>400</u>	<u>410</u>	<u>420</u>
KLIHDTNMRA	RGQPEKVFIV	NKIKTPKQID	ELIEIESDTG	TWYRRCFVRI	RTELYGIWLT
<u>430</u>	<u>440</u>	<u>450</u>	<u>460</u>	<u>470</u>	<u>480</u>
FMRCFNYPVR	ENTIKLTIWV	FTLSFGYYGL	SVWFPDVIKH	LQSDHEYALLT	RNVQKDKYAN
<u>490</u>	<u>500</u>	<u>510</u>	<u>520</u>	<u>530</u>	<u>540</u>
FSINFTEMNQ	IHTGMEYENG	RFLGVKFKSV	TFKDSVFKSC	TFDDVTSVNT	YFKNCTFIDT
<u>550</u>	<u>560</u>	<u>570</u>	<u>580</u>	<u>590</u>	<u>600</u>
LFDNTDFEPY	KFIDSEFQNC	SFLHNKTCGQ	ITFDDDDYSAY	WIYFVNFLGT	LAVLPGNIVS
<u>610</u>	<u>620</u>	<u>630</u>	<u>640</u>	<u>650</u>	<u>660</u>
ALLMDRIGRL	TMLGGSMVLS	GISCFFLWFG	TSSEMMIGML	CLYNGLTISA	WNSLDVVTVTE
<u>670</u>	<u>680</u>	<u>690</u>	<u>700</u>	<u>710</u>	<u>720</u>
LYPTDRRATG	FGFLNALCKA	AAVLGNLIFG	SLVSIKAIP	ILLASTVLVC	GGLVGLRLPD

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BLAST

ExPASy/SIB  
or at NCBI (USA)



ProtScale, Compute pI/Mw, PeptideMass,  
PeptideCutter, Dotlet (Java)



ScanProsite, MotifScan



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